

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Bandman, Olga  
Goli, Surya K.
- (ii) TITLE OF THE INVENTION: A NOVEL H-REV107-LIKE PROTEIN
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  - (B) STREET: 3174 Porter Drive
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: To Be Assigned
  - (B) FILING DATE: Filed Herewith
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Billings, Lucy J.
  - (B) REGISTRATION NUMBER: 36,749
  - (C) REFERENCE/DOCKET NUMBER: PF-0200 US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 415-855-0555
  - (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met Ala Ser Pro His Gln Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
 1             5             10             15
Phe Arg Leu Gly Tyr Glu His Trp Ala Leu Tyr Ile Gly Asp Gly Tyr
 20             25
Val Ile His Leu Ala Pro Pro Ser Glu Tyr Pro Gly Ala Gly Ser Ser
 35             40             45
Ser Val Phe Ser Val Leu Ser Asn Ser Ala Glu Val Lys Arg Glu Arg
 50             55             60
Leu Glu Asp Val Val Gly Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu
 65             70             75             80
Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala

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[illegible]

(2) INFORMATION FOR SEO ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAACAGAGAGG	AGGCACACAC	CGATCTTTGG	CTTCGAGATG	GCCTCGCCAC	ACCAAGAGGCC	60
AAACCTCGGA	GACCTGATGT	AGCTTTTTCG	CCTTGCGCTAT	GAGCAGTGGG	CGCTGTATAT	120
AGGAGATGAT	TACGTGATCC	ATCTGGCTCT	TCCAGATGTG	TACCCGCGGG	CTGGCTCTCT	180
CAGTGTCTTC	TCACTGCTGA	GCAACAGATC	AGAGGTGAAA	CGGGAGAGCT	TGGAAGATGT	240
GTGGGGAGAG	TGTTGCTATC	TGGTCAACAA	CAGCTTGGAC	CATGAGTACC	AACACGCGCC	300
CGTGGAGGTG	ATCTACAGTT	CGGCAAGAGA	GAGTGTGGAT	CAGAAGATGA	AGTACAGTAT	360
TGTGAGCAGG	TAACTGTGAG	ACTTGTGACG	CAGAGCTAGA	TATGCCAATG	CCCGCTGTAA	420
ACAGGTGAGG	AAGGCCAAGG	TCAGTGTGCG	TGTGGCCACG	TGTGGTGGAA	TCTTGTGTTT	480
TGCTGGATGT	TCTTTTNGNA	TTAGGAGATA	CCAAAGAAAA	CGCAGACGCT	GAGCAGCCCA	540
CAAAATCTCG	TGTTAGAAAG	AGCTGTGGGG	GTCCCAA			577

(2) INFORMATION FOR SEO ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
(B) CLONE: 1054752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Arg	Ala	Pro	5	Pro	Glu	Pro	Lys	Pro	Gly	Asp	Leu	Ile	Glu	Ile
1				15				10						15	
Phe	Arg	Pro	Phe	Tyr	Arg	His	Trp	Ala	Ile	Tyr	Val	Gly	Asp	Gly	Tyr
		20						25				30			
Val	Val	His	Leu	Ala	Pro	Pro	Ser	Glu	Val	Ala	Gly	Ala	Gly	Ala	Ala
		35					40					45			
Ser	Val	Met	Ser	Ala	Leu	Thr	Asp	Lys	Ala	Ile	Val	Lys	Lys	Glu	Leu
	50					55					60				
Leu	Tyr	Asp	Val	Ala	Gly	Ser	Asp	Lys	Tyr	Gln	Val	Asn	Asn	Lys	His
65					70					75					80
Asp	Asp	Lys	Tyr	Ser	Pro	Leu	Pro	Cys	Thr	Lys	Ile	Ile	Gln	Arg	Ala
			85					90						95	
Glu	Glu	Leu	Val	Gly	Gln	Glu	Val	Leu	Tyr	Lys	Leu	Thr	Ser	Glu	Asn
			100					105					110		
Cys	Glu	His	Phe	Val	Asn	Glu	Leu	Arg	Tyr	Gly	Val	Ala	Arg	Ser	Asp
		115					120					125			
Gln	Val	Arg	Asp	Val	Ile	Ile	Ala	Ala	Ser	Val	Ala	Gly	Met	Gly	Leu
	130					135					140				

Ala	Ala	Met	Ser	Leu	Ile	Gly	Val	Met	Phe	Ser	Arg	Asn	Lys	Arg	Gln
145					150					155					160
Lys	Gln														

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
 (B) CLONE: 1709969

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Pro	Ile	Pro	Glu	Pro	Lys	Pro	Gly	Asp	Leu	Ile	Glu	Ile	Phe	Arg
1				5				10						15	
Pro	Met	Tyr	Ser	His	Trp	Ala	Ile	Tyr	Val	Gly	Asp	Gly	Tyr	Val	Ile
			20					25					30		
His	Leu	Ala	Pro	Pro	Ser	Glu	Ile	Pro	Gly	Ala	Gly	Ala	Ala	Ser	Ile
		35				40						45			
Met	Ser	Ala	Leu	Thr	Asp	Lys	Ala	Ile	Val	Lys	Lys	Glu	Leu	Leu	Arg
	50					55					60				
Asp	Val	Ala	Gly	Lys	Asp	Lys	Tyr	Gln	Val	Asn	Asn	Lys	His	Asp	Lys
	65				70					75				80	
Glu	Tyr	Thr	Pro	Leu	Pro	Leu	Asn	Lys	Ile	Ile	Gln	Arg	Ala	Glu	Glu
				85				90						95	
Leu	Val	Gly	Gln	Glu	Val	Leu	Tyr	Arg	Leu	Thr	Ser	Glu	Asn	Cys	Glu
			100					105					110		
His	Phe	Val	Asn	Glu	Leu	Arg	Tyr	Gly	Val	Pro	Arg	Ser	Asp	Gln	Val
		115						120					125		
Arg	Asp	Thr	Val	Lys	Val	Ala	Thr	Val	Thr	Gly	Val	Gly	Leu	Ala	Ala
		130				135					140				
Leu	Gly	Leu	Ile	Gly	Val	Met	Leu	Ser	Arg	Asn	Lys	Lys	Gln	Lys	Gln
145					150					155					160